6. **(Twice Amended)** Method according to claim 1 further characterized in that:
step b) comprises amplifying a fragment of the protease gene with at least one 3'-primer specifically hybridizing to a target sequence located at nucleotide position 253 (codon 85) to position 300, in combination with at least one suitable 5'-primer.

12. **(Twice Amended)** A diagnostic kit enabling a method for determining the susceptibility to antiviral drugs of HIV viruses in a biological sample, with said kit comprising:

a) when appropriate, a means for releasing, isolating or concentrating the polynucleic acids present in said sample;

b) when appropriate, at least one of the primers comprising SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 or SEQ ID NO: 509; or
a 5'-primer specifically hybridizing to a target sequence located at nucleotide position 210 to 260 of the protease gene; or
a 3'-primer specifically hybridizing to a target sequence located at nucleotide position 253 (codon 85) to 300 of the protease gene;

c) at least two probes that specifically and simultaneously hybridize to a target sequence of HIV protease gene, codon 82/84, fixed to a solid support, wherein said probes are capable of simultaneously hybridizing to their respective targets under appropriate hybridization and wash conditions;

d) a hybridization buffer, or components necessary for producing said buffer;

e) a wash solution, or components necessary for producing said solution;

f) when appropriate, a means for detecting the hybrids resulting from the preceding hybridization;

g) when appropriate, a means for attaching said probe to a solid support.

13. **(Amended)** The method according to claim 1, wherein at least two probes are provided for hybridizing to each of the target sequences of codon 30; codon 46/48, codon 50; codon 54; codon 82/84 and codon 90.

17. (Amended) The kit according to claim 12, wherein at least two probes are provided for hybridizing to each of the target sequences of codon 30; codon 46/48, codon 50; codon 54; codon 82/84 and codon 90.

20. **(Amended)** A solid support for use in the method of claim 1, said support having two or more probes immobilized thereon, wherein said probes are capable of specifically and simultaneously hybridizing to a target sequence of the HIV protease gene, codon 82/84 or the complement thereof.

21. **(Amended)** The solid support of claim 25 wherein the probes are selected from the group consisting of SEQ ID NOs. 7-477.

23. **(Amended)** The solid support of claim 20 wherein the probes are selected from the group consisting of SEQ ID. NOs. 228-357.

24. **(Amended)** The solid support of claim 20 comprising SEQ ID NO. 267 and SEQ ID NO. 354.

25. **(Amended)** The solid support of claim 20 comprising at least two probes for each target sequence of codon 30, codon 46/48, codon 50, codon 54, codon 82/84, and codon 90.

26. **(Amended)** A composition comprising at least two probes fixed to a solid support for use in the method of claim 1, wherein said probes are capable of specifically and simultaneously hybridizing to a target sequence of the HIV protease gene, codon 82/84 or the complement thereof.

Please add new claims 28-33:

28. **(New)** The method according to claim 1, further comprising hybridizing at least two probes to an additional target sequence selected from the group consisting of codon 30; codon 46/48; codon 50; codon 54; and codon 90.

29. **(New)** The method according to claim 28, wherein said probes are selected from the group consisting of SEQ ID NO: 7 to SEQ ID NO: 477, SEQ ID NO: 510 to SEQ ID NO: 519 and the complements thereof.

30. **(New)** The method according to claim 1, wherein said probes are SEQ ID NO: 267 and SEQ ID NO: 354.

31. **(New)** The method according to claim 1, wherein the target sequences for codon 82/84 are shown in Figure 1.

32. **(New)** The method according to claim 13, wherein the target sequences for each codon are shown in Figure 1.

33. **(New)** The method according to claim 28, wherein the target sequences for each codon are shown in Figure 1.

REMARKS

I. Status of the claims

Claims 9 and 22 are canceled.

Claims 1, 3, 5, 6, 12, 13, 17 and 20-26 are amended and claims 28-33 are newly added.

Claims 1, 3-8, 12-21 and 23-33 are currently pending.

II. Rationale and support for the amendment of the claims

Claim 9 is canceled in response to the currently pending Restriction Requirement, as not being directed to the elected invention. Claims 1, 3, 5, 6, 12, 13, 17 and 20-26 have been amended in view of the restriction requirement to limit the inventive method to a single codon region, namely the codon region spanning 82 and 84. New claims 28 and 31-33 find support in